

In re Application of:

Cope et al.

Application No.: 10/047,253

Filed: January 14, 2002

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Amendments to the Claims:

Please amend claims 32-33, 47-48 and 74.

Please cancel claims 34-35, 39, 72 and 73.

Please add claim 77.

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-31. (Canceled)

32. (Currently amended) A method of identifying an agent that affects isopeptidase activity of a polypeptide comprising:

incubating a test agent with a polypeptide comprising a ~~JAb1/Mpn-domain Metalloenzyme (JAM)~~ Jab1/Mpn/Mov34 Metalloenzyme (JAMM) domain consisting essentially of an amino acid sequence of HXHXXXXXXXXXXXD (SEQ ID NO:1), wherein H is histidine, D is aspartate, and X is any amino acid, wherein the polypeptide having isopeptidase activity deconjugates a modifier protein from a target protein by cleaving a peptide bond formed between the carboxy terminus of the modifier protein and a free amino group of the target protein in proximity to a metal ion; and

determining the isopeptidase activity agent by measuring deconjugation of the modifier protein from the target protein polypeptide in the presence and absence of the test agent, wherein a difference in the isopeptidase activity in the presence versus the absence of the test agent is indicative of an agent that affects isopeptidase activity of the polypeptide, and wherein the polypeptide is Rpn11, or Rpn11 complex, or AMSH.

33. (Currently amended) The method of claim 32, wherein the ~~JAM~~ JAMM domain consists essentially of an amino acid sequence of GW(Y/I)H(S/T)HPXXXXXXXXSXXD (SEQ ID NO. 2), wherein G is glycine, W is tryptophan, Y is tyrosine, I is isoleucine, H is histidine, S is

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serine, T is threonine, P is proline, D is aspartate, X is any amino acid, Y/I is either Y or I, and S/T is either S or T.

34. (Canceled)

35. (Canceled)

36. (Original) The method of claim 32, wherein the target protein has ubiquitin ligase activity.

37. (Original) The method of claim 32, wherein the target protein is part of a protein complex having ubiquitin ligase activity.

38. (Canceled)

39. (Canceled)

40. (Canceled)

41. (Previously Presented) The method of claim 32, wherein an increase in the amount of the target protein not conjugated to the modifier protein is indicative of an agent that increases deconjugation of the modifier protein from the target protein.

42. (Original) The method of claim 32, wherein the target protein has the activity of peroxidase, alkaline phosphatase, or luciferase.

43. (Original) The method of claim 32, wherein the target protein is a fluorescent protein.

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44. (Original) The method of claim 43, wherein the fluorescent protein is selected from the group consisting of green fluorescent protein, yellow fluorescent protein, cyan fluorescent protein and dsRed.
45. (Original) The method of claim 43, wherein the target protein is a fluorescent protein via chemical modification.
46. (Original) The method of claim 32, wherein the target protein causes production of a detectable signal upon deconjugation from the modifier protein.
47. (Currently amended) The method of claim 32, wherein the polypeptide Rpn11 is a polypeptide complex of 26S proteasome.
48. (Currently amended) The method of claim 32, wherein the polypeptide Rpn11 is a polypeptide complex of 26S proteasome and the modifier protein is an ubiquitin.
49. (Original) The method of claim 47, wherein the incubation is conducted in the presence and absence of the test agent, the target protein, the 26S proteasome, and a 20S inhibitor.
50. (Original) The method of claim 47, wherein the incubation is conducted in the presence and absence of the test agent, the target protein, the 26S proteasome, a 20S inhibitor, and ATP.
51. (Original) The method of claim 50, wherein the incubation further includes an inhibitor of deubiquitination by an ubiquitin isopeptidase.
52. (Original) The method of claim 47, wherein the target protein not conjugated to the modifier protein is not degraded.

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53. (Original) The method of claim 47, wherein the target protein is Sic1.
54. (Original) The method of claim 47, wherein the 26S proteasome is purified from *S. cerevisiae*.
55. (Original) The method of claim 47, wherein the 26S proteasome is purified from eukaryotic cells.
56. (Original) The method of claim 47, wherein the 26S proteasome is purified from human cells.
57. (Original) The method of claim 32, wherein the test agent is a member of a compound library selected from the group consisting of hydroxamate compound library, reverse hydroxamate compound library, carboxylate compound library, thiol compound library, and phosphonate compound library.
- 58-71. (Canceled)
72. (Canceled)
73. (Canceled)
74. (Currently Amended) The method of claim ~~72~~ 32, wherein the method further comprises carrying out the incubation in the presence of an inhibitor of degradation of the target protein.
75. (Previously Presented) The method of claim 32, further comprising after the incubation, determining whether the modifier protein remains conjugated to the target protein via

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a peptide bond formed between the carboxy terminus of the modifier protein and a free amino group of the target protein.

76. (Canceled)

77. (New) The method of claim 32, wherein the polypeptide comprising the JAMM domain comprises AMSH1 and/or AMSH2.

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